

5021US_SEQ.TXT

SEQUENCE LISTING

<110> Cowan, Conrad L.

<120> METHODS OF SCREENING COMPOSITIONS FOR G
PROTEIN-COUPLED RECEPTOR AGONIST ACTIVITY

<130> 067437-5021-US

<140> US 10/572,529

<141> 2007-03-05

<150> PCT/US2004/030261

<151> 2004-09-16

<150> US 60/503,447

<151> 2003-09-16

<160> 59

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 43

<212> PRT

<213> Homo sapiens

<400> 1

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Asn Pro Ile Val Tyr Ala Phe Arg Ile Gln Lys Phe Arg Val Thr Phe
 1           5           10           15
Leu Lys Ile Trp Asn Asp His Phe Arg Cys Gln Pro Ala Pro Pro Ile
          20           25           30
Asp Glu Asp Leu Pro Glu Glu Arg Pro Asp Asp
      35           40

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<210> 2

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<212> PRT

<213> Homo sapiens

<400> 2

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Asn Pro Ile Ile Tyr Pro Cys Ser Ser Lys Glu Phe Lys Arg Ala Phe
 1           5           10           15
Val Arg Ile Leu Gly Cys Gln Cys Arg Gly Arg Gly Arg Arg Arg
          20           25           30
Arg Arg Arg Arg Arg Leu Gly Gly Cys Ala Tyr Thr Tyr Arg Pro Trp
      35           40           45
Thr Arg Gly Gly Ser Leu Glu Arg Ser Gln Ser Arg Lys Asp Ser Leu
      50           55           60
Asp Asp Ser Gly Ser Cys Leu Ser Gly Ser Gln Arg Thr Leu Pro Ser
      65           70           75           80
Ala Ser Pro Ser Pro Gly Tyr Leu Gly Arg Gly Ala Pro Pro Pro Val
          85           90           95
Glu Leu Cys Ala Phe Pro Glu Trp Lys Ala Pro Gly Ala Leu Leu Ser
      100           105           110
Leu Pro Ala Pro Glu Pro Pro Gly Arg Arg Gly Arg His Asp Ser Gly
      115           120           125
Pro Leu Phe Thr Phe Lys Leu Leu Thr Glu Pro Glu Ser Pro Gly Thr
      130           135           140
Asp Gly Gly Ala Ser Asn Gly Gly Cys Glu Ala Ala Asp Val Ala

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145 Asn Gly Gln Pro Gly Phe Lys Ser Asn Met Pro Leu Ala Pro Gly Gln
150 155 160
165 170 175

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1 5 10 15
Lys Lys Ile Leu Cys Arg Gly Asp Arg Lys Arg Ile Val
20 25

<400> 4
Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp Phe Arg Arg Ala Phe
1 5 10 15
Arg Arg Ile Leu Cys Arg Pro Trp Thr Gln Thr Ala Trp
20 25

<400> 5
Asn Pro Val Ile Tyr Thr Val Phe Asn Gln Asp Phe Arg Pro Ser Phe
1 5 10 15
Lys His Ile Leu Phe Arg Arg Arg Arg Gly Phe Arg Gln
20 25 30

<400>	6															
Asn	Pro	Ile	Ile	Tyr	Cys	Arg	Ser	Pro	Asp	Phe	Arg	Lys	Ala	Phe	Gln	
1				5					10					15		
Gly	Leu	Leu	Cys	Cys	Ala	Arg	Arg	Ala	Ala	Arg	Arg	Arg	His	Ala	Thr	
			20					25					30			
His	Gly	Asp	Arg	Pro	Arg	Ala	Ser	Gly	Cys	Leu	Ala	Arg	Pro	Gly	Pro	
		35					40					45				
Pro	Pro	Ser	Pro	Gly	Ala	Ala	Ser	Asp	Asp	Asp	Asp	Asp	Asp	Val	Val	
	50					55					60					
Gly	Ala	Thr	Pro	Pro	Ala	Arg	Leu	Leu	Glu	Pro	Trp	Ala	Gly	Cys	Asn	
65					70					75					80	
Gly	Gly	Ala	Ala	Ala	Asp	Ser	Asp	Ser	Ser	Leu	Asp	Glu	Pro	Cys	Arg	
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Pro	Gly	Phe	Ala	Ser	Glu	Ser	Lys	Val								
			100					105								

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 <213> Homo sapiens

<400> 7
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 Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys Ala Tyr Gly Asn Gly
 20 25 30
 Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser Gly Tyr His Val Glu
 35 40 45
 Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp Leu Pro Gly Thr Glu
 50 55 60
 Asp Phe Val Gly His Gln Gly Thr Val Pro Ser Asp Asn Ile Asp Ser
 65 70 75 80
 Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu Leu
 85 90

<210> 8
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 <212> PRT
 <213> Homo sapiens

<400> 8
 Asn Pro Ile Ile Tyr Ala Phe Asn Ala Asp Phe Arg Lys Ala Phe Ser
 1 5 10 15
 Thr Leu Leu Gly Cys Tyr Arg Leu Cys Pro Ala Thr Asn Asn Ala Ile
 20 25 30
 Glu Thr Val Ser Ile Asn Asn Asn Gly Ala Ala Met Phe Ser Ser His
 35 40 45
 His Glu Pro Arg Gly Ser Ile Ser Lys Glu Cys Asn Leu Val Tyr Leu
 50 55 60
 Ile Pro His Ala Val Gly Ser Ser Glu Asp Leu Lys Lys Glu Glu Ala
 65 70 75 80
 Ala Gly Ile Ala Arg Pro Leu Glu Lys Leu Ser Pro Ala Leu Ser Val
 85 90 95
 Ile Leu Asp Tyr Asp Thr Asp Val Ser Leu Glu Lys Ile Gln Pro Ile
 100 105 110
 Thr Gln Asn Gly Gln His Pro Thr
 115 120

<210> 9
 <211> 22
 <212> PRT
 <213> Homo sapiens

<400> 9
 Asn Pro Ile Ile Tyr Thr Thr Phe Asn Ile Glu Phe Arg Lys Ala Phe
 1 5 10 15
 Leu Lys Ile Leu His Cys
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<210> 10
 <211> 22
 <212> PRT
 <213> Homo sapiens

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<400> 10

Asn Pro Val Ile Tyr Thr Thr Phe Asn Ile Glu Phe Arg Lys Ala Phe
 1 5 10 15
 Leu Lys Ile Leu Ser Cys
 20

<210> 11

<211> 24

<212> PRT

<213> Homo sapiens

<400> 11

Asn Pro Val Ile Tyr Thr Val Phe Asn Ala Glu Phe Arg Asn Val Phe
 1 5 10 15
 Arg Lys Ala Leu Arg Ala Cys Cys
 20

<210> 12

<211> 123

<212> PRT

<213> Homo sapiens

<400> 12

Asn Pro Val Ile Tyr Ala Phe Asn Ala Asp Phe Gln Lys Val Phe Ala
 1 5 10 15
 Gln Leu Leu Gly Cys Ser His Phe Cys Ser Arg Thr Pro Val Glu Thr
 20 25 30
 Val Asn Ile Ser Asn Glu Leu Ile Ser Tyr Asn Gln Asp Ile Val Phe
 35 40 45
 His Lys Glu Ile Ala Ala Ala Tyr Ile His Met Met Pro Asn Ala Val
 50 55 60
 Thr Pro Gly Asn Arg Glu Val Asp Asn Asp Glu Glu Glu Gly Pro Phe
 65 70 75 80
 Asp Arg Met Phe Gln Ile Tyr Gln Thr Ser Pro Asp Gly Asp Pro Val
 85 90 95
 Ala Glu Ser Val Trp Glu Leu Asp Cys Glu Gly Glu Ile Ser Leu Asp
 100 105 110
 Lys Ile Thr Pro Phe Thr Pro Asn Gly Phe His
 115 120

<210> 13

<211> 47

<212> PRT

<213> Homo sapiens

<400> 13

Asn Pro Met Cys Tyr Ala Leu Cys Asn Lys Ala Phe Arg Asp Thr Phe
 1 5 10 15
 Arg Leu Leu Leu Cys Arg Trp Asp Lys Arg Arg Trp Arg Lys Ile
 20 25 30
 Pro Lys Arg Pro Gly Ser Val His Arg Thr Pro Ser Arg Gln Cys
 35 40 45

<210> 14

<211> 31

<212> PRT

<213> Homo sapiens

<400> 14

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Asn Pro Ala Cys Tyr Ala Leu Cys Asn Ala Thr Phe Lys Lys Thr Phe
 1 5 10 15
 Lys His Leu Leu Met Cys His Tyr Lys Asn Ile Gly Ala Thr Arg
 20 25 30

<210> 15
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 15
 Asn Pro Val Cys Tyr Ala Leu Cys Asn Lys Thr Phe Arg Thr Thr Phe
 1 5 10 15
 Lys Met Leu Leu Leu Cys Gln Cys Asp Lys Lys Lys Arg Arg Lys Gln
 20 25 30
 Gln Tyr Gln Gln Arg Gln Ser Val Ile Phe His Lys Arg Ala Pro Glu
 35 40 45
 Gln Ala Leu
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<210> 16
 <211> 31
 <212> PRT
 <213> Homo sapiens

<400> 16
 Asn Pro Ala Cys Tyr Ala Leu Cys Asn Ala Thr Phe Lys Lys Thr Phe
 1 5 10 15
 Arg His Leu Leu Leu Cys Gln Tyr Arg Asn Ile Gly Thr Ala Arg
 20 25 30

<210> 17
 <211> 42
 <212> PRT
 <213> Homo sapiens

<400> 17
 Asn Pro Ile Cys Tyr Ala Leu Cys Asn Arg Thr Phe Arg Lys Thr Phe
 1 5 10 15
 Lys Met Leu Leu Leu Cys Arg Trp Lys Lys Lys Lys Val Glu Glu Lys
 20 25 30
 Leu Tyr Trp Gln Gly Asn Ser Lys Leu Pro
 35 40

<210> 18
 <211> 24
 <212> PRT
 <213> Homo sapiens

<400> 18
 Asn Pro Val Ile Tyr Ala Tyr Phe Asn Lys Asp Phe Gln Asn Ala Phe
 1 5 10 15
 Lys Lys Ile Ile Lys Cys Lys Phe
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<210> 19
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 <212> PRT

5021US_SEQ.TXT

<213> Homo sapiens

<400> 19

Asn Pro Ile Ile Tyr Thr Met Ser Asn Glu Asp Phe Lys Gln Ala Phe
 1 5 10 15
 His Lys Leu Ile Arg Phe Lys Cys Thr Ser
 20 25

<210> 20

<211> 24

<212> PRT

<213> Homo sapiens

<400> 20

Asn Pro Leu Leu Tyr Thr Ser Phe Asn Glu Asp Phe Lys Leu Ala Phe
 1 5 10 15
 Lys Lys Leu Ile Arg Cys Arg Glu
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<210> 21

<211> 37

<212> PRT

<213> Homo sapiens

<400> 21

Asn Pro Ile Ile Tyr Cys Leu Arg Asn Gln Glu Val Lys Arg Ala Leu
 1 5 10 15
 Cys Cys Ile Leu His Leu Tyr Gln His Gln Asp Pro Asp Pro Lys Lys
 20 25 30
 Gly Ser Arg Asn Val
 35

<210> 22

<211> 27

<212> PRT

<213> Homo sapiens

<400> 22

Asn Pro Leu Ile Tyr Thr Leu Arg Asn Met Glu Val Lys Gly Ala Leu
 1 5 10 15
 Arg Arg Leu Leu Gly Lys Gly Arg Glu Val Gly
 20 25

<210> 23

<211> 62

<212> PRT

<213> Homo sapiens

<400> 23

Asn Pro Leu Phe Tyr Gly Phe Leu Gly Lys Lys Phe Lys Arg Tyr Phe
 1 5 10 15
 Leu Gln Leu Leu Lys Tyr Ile Pro Pro Lys Ala Lys Ser His Ser Asn
 20 25 30
 Leu Ser Thr Lys Met Ser Thr Leu Ser Tyr Arg Pro Ser Asp Asn Val
 35 40 45
 Ser Ser Ser Thr Lys Lys Pro Ala Pro Cys Phe Glu Val Glu
 50 55 60

5021US_SEQ.TXT

<210> 24
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 <212> PRT
 <213> Homo sapiens

<400> 24
 Asn Pro Phe Leu Tyr Cys Phe Val Gly Asn Arg Phe Gln Gln Lys Leu
 1 5 10 15
 Arg Ser Val Phe Arg Val Pro Ile Thr Trp Leu Gln Gly Lys Arg Glu
 20 25 30
 Ser Met Ser Cys Arg Lys Ser Ser Leu Arg Glu Met Glu Thr Phe
 35 40 45
 Val Ser
 50

<210> 25
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 25
 Asn Pro Leu Ile Tyr Ala Phe Ile Gly Gln Lys Phe Arg His Gly Leu
 1 5 10 15
 Leu Lys Ile Leu Ala Ile His Gly Leu Ile Ser Lys Asp Ser Leu Pro
 20 25 30
 Lys Asp Ser Arg Pro Ser Phe Val Gly Ser Ser Ser Gly His Thr Ser
 35 40 45
 Thr Thr Leu
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<210> 26
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 26
 Asn Pro Leu Ile Tyr Ala Phe Ala Gly Glu Lys Phe Arg Arg Tyr Leu
 1 5 10 15
 Tyr His Leu Tyr Gly Lys Cys Leu Ala Val Leu Cys Gly Arg Ser Val
 20 25 30
 His Val Asp Phe Ser Ser Ser Glu Ser Gln Arg Ser Arg His Gly Ser
 35 40 45
 Val Leu Ser Ser Asn Phe Thr Tyr His Thr Ser Asp Gly Asp Ala Leu
 50 55 60
 Leu Leu Leu
 65

<210> 27
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 27
 Asn Pro Ile Leu Tyr Asn Leu Val Ser Ala Asn Phe Arg His Ile Phe
 1 5 10 15
 Leu Ala Thr Leu Ala Cys Leu Cys Pro Val Trp Arg Arg Arg Arg Lys
 20 25 30
 Arg Pro Ala Phe Ser Arg Lys Ala Asp Ser Val Ser Ser Asn His Thr
 35 40 45
 Leu Ser Ser Asn Ala Thr Arg Glu Thr Leu Tyr

50

55

<210> 28
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 28
 Asn Pro Ile Ile Tyr Cys Cys Leu Asn Asp Arg Phe Arg Leu Gly Phe
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 Lys His Ala Phe Arg Cys Cys Pro Phe Ile Ser Ala Gly Asp Tyr Glu
 20 25 30
 Gly Leu Glu Met Lys Ser Thr Arg Tyr Leu Gln Thr Gln Gly Ser Val
 35 40 45
 Tyr Lys Val Ser Arg Leu Glu Thr Thr Ile Ser Thr Val Val Gly Ala
 50 55 60
 His Glu Glu Glu Pro Glu Asp Gly Pro Lys Ala Thr Pro Ser Ser Leu
 65 70 75 80
 Asp Leu Thr Ser Asn Cys Ser Ser Arg Ser Asp Ser Lys Thr Met Thr
 85 90 95
 Glu Ser Phe Ser Phe Ser Ser Asn Val Leu Ser
 100 105

<210> 29
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 29
 Asn Pro Trp Ile Tyr Ala Ser Phe Ser Ser Ser Val Ser Ser Glu Leu
 1 5 10 15
 Arg Ser Leu Leu Cys Cys Ala Arg Gly Arg Thr Pro Pro Ser Leu Gly
 20 25 30
 Pro Gln Asp Glu Ser Cys Thr Thr Ala Ser Ser Ser Leu Ala Lys Asp
 35 40 45
 Thr Ser Ser
 50

<210> 30
 <211> 83
 <212> PRT
 <213> Homo sapiens

<400> 30
 Asn Pro Val Ile Tyr Asn Leu Met Ser Gln Lys Phe Arg Ala Ala Phe
 1 5 10 15
 Arg Lys Leu Cys Asn Cys Lys Gln Lys Pro Thr Glu Lys Pro Ala Asn
 20 25 30
 Tyr Ser Val Ala Leu Asn Tyr Ser Val Ile Lys Glu Ser Asp His Phe
 35 40 45
 Ser Thr Glu Leu Asp Asp Ile Thr Val Thr Asp Thr Tyr Leu Ser Ala
 50 55 60
 Thr Lys Val Ser Phe Asp Asp Thr Cys Leu Ala Ser Glu Val Ser Phe
 65 70 75 80
 Ser Gln Ser

<210> 31
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5021US_SEQ.TXT

<212> PRT

<213> Homo sapiens

<400> 31

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Asn Pro Trp Ile Tyr Met Leu Phe Thr Gly His Leu Phe His Glu Leu
 1      5      10      15
Val Gln Arg Phe Leu Cys Cys Ser Ala Ser Tyr Leu Lys Gly Arg Arg
 20      25      30
Leu Gly Glu Thr Ser Ala Ser Lys Lys Ser Asn Ser Ser Ser Phe Val
 35      40      45
Leu Ser His Arg Ser Ser Ser Gln Arg Ser Cys Ser Gln Pro Ser Thr
 50      55      60
Ala
65

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<210> 32

<211> 75

<212> PRT

<213> Homo sapiens

<400> 32

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Asn Pro Val Leu Tyr Ser Leu Met Ser Ser Arg Phe Arg Glu Thr Phe
 1      5      10      15
Gln Glu Ala Leu Cys Leu Gly Ala Cys Cys His Arg Leu Arg Pro Arg
 20      25      30
His Ser Ser His Ser Leu Ser Arg Met Thr Thr Gly Ser Thr Leu Cys
 35      40      45
Asp Val Gly Ser Leu Gly Ser Trp Val His Pro Leu Ala Gly Asn Asp
 50      55      60
Gly Pro Glu Ala Gln Gln Glu Thr Asp Pro Ser
65      70      75

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<210> 33

<211> 62

<212> PRT

<213> Homo sapiens

<400> 33

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Asn Pro Leu Val Tyr Cys Phe Met His Arg Arg Phe Arg Gln Ala Cys
 1      5      10      15
Leu Glu Thr Cys Ala Arg Cys Cys Pro Arg Pro Pro Arg Ala Arg Pro
 20      25      30
Arg Ala Leu Pro Asp Glu Asp Pro Pro Thr Pro Ser Ile Ala Ser Leu
 35      40      45
Ser Arg Leu Ser Tyr Thr Thr Ile Ser Thr Leu Gly Pro Gly
 50      55      60

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<210> 34

<211> 82

<212> PRT

<213> Homo sapiens

<400> 34

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Asn Pro Leu Val Tyr Ala Leu Ala Ser Arg His Phe Arg Ala Arg Phe
 1      5      10      15
Arg Arg Leu Trp Pro Cys Gly Arg Arg Arg His Arg Ala Arg Arg
 20      25      30
Ala Leu Arg Arg Val Arg Pro Ala Ser Ser Gly Pro Pro Gly Cys Pro
 35      40      45
Gly Asp Ala Arg Pro Ser Gly Arg Leu Leu Ala Gly Gly Gly Gln Gly

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 Pro Glu Pro Arg Glu Gly Pro Val His Gly Gly Glu Ala Ala Arg Gly
 65 70 75 80
 Pro Glu

<210> 35
 <211> 76
 <212> PRT
 <213> Homo sapiens

<400> 35
 Asn Pro Ile Ile Tyr Thr Leu Thr Asn Lys Glu Met Arg Arg Ala Phe
 1 5 10 15
 Ile Arg Ile Met Ser Cys Cys Lys Cys Pro Ser Gly Asp Ser Ala Gly
 20 25 30
 Lys Phe Lys Arg Pro Ile Ile Ala Gly Met Glu Phe Ser Arg Ser Lys
 35 40 45
 Ser Asp Asn Ser Ser His Pro Gln Lys Asp Glu Gly Asp Asn Pro Glu
 50 55 60
 Thr Ile Met Ser Ser Gly Asn Val Asn Ser Ser Ser
 65 70 75

<210> 36
 <211> 80
 <212> PRT
 <213> Homo sapiens

<400> 36
 Asn Pro Ile Ile Tyr Ala Leu Arg Ser Lys Asp Leu Arg His Ala Phe
 1 5 10 15
 Arg Ser Met Phe Pro Ser Cys Glu Gly Thr Ala Gln Pro Leu Asp Asn
 20 25 30
 Ser Met Gly Asp Ser Asp Cys Leu His Lys His Ala Asn Asn Ala Ala
 35 40 45
 Ser Val His Arg Ala Ala Glu Ser Cys Ile Lys Ser Thr Val Lys Ile
 50 55 60
 Ala Lys Val Thr Met Ser Val Ser Thr Asp Thr Ser Ala Glu Ala Leu
 65 70 75 80

<210> 37
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 37
 Asn Pro Val Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe
 1 5 10 15
 Arg Gln Leu Cys Arg Lys Pro Cys Gly Arg Pro Asp Pro Ser Ser Phe
 20 25 30
 Ser Arg Pro Arg Glu Ala Thr Ala Arg Glu Arg Val Thr Ala Cys Thr
 35 40 45
 Pro Ser Asp Gly Pro Gly Gly Gly Arg Ala Ala
 50 55

<210> 38
 <211> 58
 <212> PRT
 <213> Homo sapiens

5021US_SEQ.TXT

<400> 38

Asp Pro Phe Val Tyr Tyr Phe Val Ser His Asp Phe Arg Asp His Ala
 1 5 10 15
 Lys Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val Lys Gln Met Gln
 20 25 30
 Val Ser Leu Thr Ser Lys Lys His Ser Arg Lys Ser Ser Tyr Ser
 35 40 45
 Ser Ser Ser Thr Thr Val Lys Thr Ser Tyr
 50 55

<210> 39

<211> 66

<212> PRT

<213> Rattus norvegicus

<400> 39

Asn Gly Glu Val Gln Ala Glu Leu Arg Arg Lys Trp Arg Arg Trp His
 1 5 10 15
 Leu Gln Gly Val Leu Gly Trp Ser Ser Lys Ser Gln His Pro Trp Gly
 20 25 30
 Gly Ser Asn Gly Ala Thr Cys Ser Thr Gln Val Ser Met Leu Thr Arg
 35 40 45
 Val Ser Pro Ser Ala Arg Arg Ser Ser Ser Phe Gln Ala Glu Val Ser
 50 55 60
 Leu Val
 65

<210> 40

<211> 346

<212> PRT

<213> Artificial Sequence

<220>

<223> hGPR3- Enhanced Receptor

<400> 40

Met Met Trp Gly Ala Gly Ser Pro Leu Ala Trp Leu Ser Ala Gly Ser
 1 5 10 15
 Gly Asn Val Asn Val Ser Ser Val Gly Pro Ala Glu Gly Pro Thr Gly
 20 25 30
 Pro Ala Ala Pro Leu Pro Ser Pro Lys Ala Trp Asp Val Val Leu Cys
 35 40 45
 Ile Ser Gly Thr Leu Val Ser Cys Glu Asn Ala Leu Val Val Ala Ile
 50 55 60
 Ile Val Gly Thr Pro Ala Phe Arg Ala Pro Met Phe Leu Leu Val Gly
 65 70 75 80
 Ser Leu Ala Val Ala Asp Leu Leu Ala Gly Leu Gly Leu Val Leu His
 85 90 95
 Phe Ala Ala Val Phe Cys Ile Gly Ser Ala Glu Met Ser Leu Val Leu
 100 105 110
 Val Gly Val Leu Ala Met Ala Phe Thr Ala Ser Ile Gly Ser Leu Leu
 115 120 125
 Ala Ile Thr Val Asp Arg Tyr Leu Ser Leu Tyr Asn Ala Leu Thr Tyr
 130 135 140
 Tyr Ser Glu Thr Thr Val Thr Arg Thr Tyr Val Met Leu Ala Leu Val
 145 150 155 160
 Trp Gly Gly Ala Leu Gly Leu Gly Leu Leu Pro Val Leu Ala Trp Asn
 165 170 175
 Cys Leu Asp Gly Leu Thr Thr Cys Gly Val Val Tyr Pro Leu Ser Lys
 180 185 190

5021US_SEQ.TXT

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Asn His Leu Val Val Leu Ala Ile Ala Phe Phe Met Val Phe Gly Ile
195      200      205
Met Leu Gln Leu Tyr Ala Gln Ile Cys Arg Ile Val Cys Arg His Ala
210      215      220
Gln Gln Ile Ala Leu Gln Arg His Leu Leu Pro Ala Ser His Tyr Val
225      230      235
Ala Thr Arg Lys Gly Ile Ala Thr Leu Ala Val Val Leu Gly Ala Phe
245      250      255
Ala Ala Cys Trp Leu Pro Phe Thr Val Tyr Cys Leu Leu Gly Asp Ala
260      265      270
His Ser Pro Pro Leu Tyr Thr Tyr Leu Thr Leu Leu Pro Ala Thr Tyr
275      280      285
Asn Ser Met Ile Asn Pro Ile Ile Tyr Ala Phe Arg Asn Gln Asp Val
290      295      300
Gln Lys Val Leu Trp Ala Val Cys Cys Cys Cys Ala Ala Ala Arg Gly
305      310      315
Arg Thr Pro Pro Ser Leu Gly Pro Gln Asp Glu Ser Cys Thr Thr Ala
325      330      335
Ser Ser Ser Leu Ala Lys Asp Thr Ser Ser
340      345

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<210> 41
 <211> 1041
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> hGPR3- Enhanced Receptor

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<400> 41
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gtaagcagcg tgggcccagc agagggggccc acaggtccag ccgcaccact gccctcgcct 120
aaggcctggg atgtggtgct ctgcatctca ggcaccctgg tgtcctgcga gaatgcgcta 180
gtggtggcca tcatcgtagg cactcctgcc ttccgtgccc ccatgttcct gctggtgggc 240
agcctggccg tggcagacct gctggcaggc ctgggcctgg tcctgcactt tgctgctgtc 300
ttctgcatcg gctcagcgga gatgagcttg gtgctggttg gcgtgctggc aatggccttt 360
actgccagca tcggcagttc actggccatc actgtcgacc gctacctttc tctgtacaat 420
gccctcacct actattcaga gacaacagtg acacggacct atgtgatgct ggccttagtg 480
tggggagggtg ccctgggcct ggggctgctg cctgtgctgg cctggaactg cctggatggc 540
ctgaccacat gtggcgtggt ttatccactc tccaagaacc atctggtagt tctggccatt 600
gccttcttca tgggtgtttg catcatgctg cagctctacg ccaaatctg ccgcatcgct 660
tgccgccatg cccagcagat tgcccttcag cggcacctgc tgcctgcctc ccactatgtg 720
gccacccgca agggcattgc cacactggcc gtggtgcttg gagcctttgc cgctgctgg 780
ttgcccttca ctgtctactg cctgctgggt gatgcccact ctccacctct ctacacctat 840
cttaccttgc tccctgccac ctacaactcc atgatcaacc ctatcatcta cgcttccgc 900
aaccaggatg tgcagaaagt gctgtgggct gtctgtgctg gctgtgcggc cgcacgggga 960
cgcacccacg ccagcctggg tccccaagat gagtccctga ccaccgccag ctctccctg 1020
gccaaaggaca cttcatcgta a
1041

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<210> 42
 <211> 378
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hGPR6- Enhanced Receptor

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<400> 42
Met Asn Ala Ser Ala Ala Ser Leu Asn Asp Ser Gln Val Val Val Val
1      5      10      15
Ala Ala Glu Gly Ala Ala Ala Ala Ala Thr Ala Ala Gly Gly Pro Asp
20      25      30

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5021US_SEQ.TXT

Thr Gly Glu Trp Gly Pro Pro Ala Ala Ala Ala Leu Gly Ala Gly Gly
 35 40 45
 Gly Ala Asn Gly Ser Leu Glu Leu Ser Ser Gln Leu Ser Ala Gly Pro
 50 55 60
 Pro Gly Leu Leu Leu Pro Ala Val Asn Pro Trp Asp Val Leu Leu Cys
 65 70 75 80
 Val Ser Gly Thr Val Ile Ala Gly Glu Asn Ala Leu Val Val Ala Leu
 85 90 95
 Ile Ala Ser Thr Pro Ala Leu Arg Thr Pro Met Phe Val Leu Val Gly
 100 105 110
 Ser Leu Ala Thr Ala Asp Leu Leu Ala Gly Cys Gly Leu Ile Leu His
 115 120 125
 Phe Val Phe Gln Tyr Leu Val Pro Ser Glu Thr Val Ser Leu Leu Thr
 130 135 140
 Val Gly Phe Leu Val Ala Ser Phe Ala Ala Ser Val Ser Ser Leu Leu
 145 150 155 160
 Ala Ile Thr Val Asp Arg Tyr Leu Ser Leu Tyr Asn Ala Leu Thr Tyr
 165 170 175
 Tyr Ser Arg Arg Thr Leu Leu Gly Val His Leu Leu Leu Ala Ala Thr
 180 185 190
 Trp Thr Val Ser Leu Gly Leu Gly Leu Leu Pro Val Leu Gly Trp Asn
 195 200 205
 Cys Leu Ala Glu Arg Ala Ala Cys Ser Val Val Arg Pro Leu Ala Arg
 210 215 220
 Ser His Val Ala Leu Leu Ser Ala Ala Phe Phe Met Val Phe Gly Ile
 225 230 235 240
 Met Leu His Leu Tyr Val Arg Ile Cys Gln Val Val Trp Arg His Ala
 245 250 255
 His Gln Ile Ala Leu Gln Gln His Cys Leu Ala Pro Pro His Leu Ala
 260 265 270
 Ala Thr Arg Lys Gly Val Gly Thr Leu Ala Val Val Leu Gly Thr Phe
 275 280 285
 Gly Ala Ser Trp Leu Pro Phe Ala Ile Tyr Cys Val Val Gly Ser His
 290 295 300
 Glu Asp Pro Ala Val Tyr Thr Tyr Ala Thr Leu Leu Pro Ala Thr Tyr
 305 310 315 320
 Asn Ser Met Ile Asn Pro Ile Ile Tyr Ala Phe Arg Asn Gln Glu Ile
 325 330 335
 Gln Arg Ala Leu Trp Leu Leu Leu Cys Gly Cys Ala Ala Ala Arg Gly
 340 345 350
 Arg Thr Pro Pro Ser Leu Gly Pro Gln Asp Glu Ser Cys Thr Thr Ala
 355 360 365
 Ser Ser Ser Leu Ala Lys Asp Thr Ser Ser
 370 375

<210> 43

<211> 1137

<212> DNA

<213> Artificial Sequence

<220>

<223> hGPR6- Enhanced Receptor

<400> 43

atgaacgcga ggcgcgcctc gctcaacgac tcccaggtgg tggtagtggc ggccgaagga 60
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 gcggcggcctc taggagccgg cggcggaagt aatgggtctc tggagctgtc ctgcagctg 180
 tcggctgggc caccgggact cctgctgcca gcggtgaatc cgtgggacgt gctcctgtgc 240
 gtgtcgggga cagtgatcgc tggagaaaac gcgctggtgg tggcgctcat cgcgtccact 300
 ccggcgctgc gcacgcccat gttcgtgctg gtaggcagcc tggccaccgc tgacctgttg 360
 gcgggctgtg gcctcatctt gcactttgtg ttccagtact tggcgccctc ggagactgtg 420
 agtctgctca cgggtgggctt cctcgtggcc tccttcgccg cctctgtcag cagcctgctg 480

5021US_SEQ.TXT

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gccattacgg tggaccgcta cctgtccctg tataacgcgc tcacctatta ctgcgcgccg 540
accctgttgg gcgtgcacct cctgcttgcc gccacttgga ccgtgtccct aggcctgggg 600
ctgctgcccg tgctgggctg gaactgcctg gcagagcgcg ccgcctgcag cgtgggtgcg 660
ccgctggcgc gcagccacgt ggctctgctc tccgccgcct tcttcatggg cttcggcatc 720
atgctgcacc tgtacgtgcg catctgccag gtggtctggc gccacgcgca ccagatcgcg 780
ctgcagcagc actgcctggc gccaccccat ctgcctgcca ccagaaaggg tgggggtaca 840
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gtgggcagcc atgaggaccc ggcgggtctac acttacgcca ccctgctgcc cgccacctac 960
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tggctcctgc tctgtggctg tgcggccgca cggggacgca cccacccag cctgggtccc 1080
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```

<210> 44

<211> 350

<212> PRT

<213> Artificial Sequence

<220>

<223> hGPR12- Enhanced Receptor

<400> 44

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Met Asn Glu Asp Leu Lys Val Asn Leu Ser Gly Leu Pro Arg Asp Tyr
1      5      10      15
Leu Asp Ala Ala Ala Glu Asn Ile Ser Ala Ala Val Ser Ser Arg
20      25      30
Val Pro Ala Val Glu Pro Glu Pro Glu Leu Val Val Asn Pro Trp Asp
35      40      45
Ile Val Leu Cys Thr Ser Gly Thr Leu Ile Ser Cys Glu Asn Ala Ile
50      55      60
Val Val Leu Ile Ile Phe His Asn Pro Ser Leu Arg Ala Pro Met Phe
65      70      75      80
Leu Leu Ile Gly Ser Leu Ala Leu Ala Asp Leu Leu Ala Gly Ile Gly
85      90      95
Leu Ile Thr Asn Phe Val Phe Ala Tyr Leu Leu Gln Ser Glu Ala Thr
100     105     110
Lys Leu Val Thr Ile Gly Leu Ile Val Ala Ser Phe Ser Ala Ser Val
115     120     125
Cys Ser Leu Leu Ala Ile Thr Val Asp Arg Tyr Leu Ser Leu Tyr Tyr
130     135     140
Ala Leu Thr Tyr His Ser Glu Arg Thr Val Thr Phe Thr Tyr Val Met
145     150     155     160
Leu Val Met Leu Trp Gly Thr Ser Ile Cys Leu Gly Leu Leu Pro Val
165     170     175
Met Gly Trp Asn Cys Leu Arg Asp Glu Ser Thr Cys Ser Val Val Arg
180     185     190
Pro Leu Thr Lys Asn Asn Ala Ala Ile Leu Ser Val Ser Phe Leu Phe
195     200     205
Met Phe Ala Leu Met Leu Gln Leu Tyr Ile Gln Ile Cys Lys Ile Val
210     215     220
Met Arg His Ala His Gln Ile Ala Leu Gln His His Phe Leu Ala Thr
225     230     235     240
Ser His Tyr Val Thr Arg Lys Gly Val Ser Thr Leu Ala Ile Ile
245     250     255
Leu Gly Thr Phe Ala Ala Cys Trp Met Pro Phe Thr Leu Tyr Ser Leu
260     265     270
Ile Ala Asp Tyr Thr Tyr Pro Ser Ile Tyr Thr Tyr Ala Thr Leu Leu
275     280     285
Pro Ala Thr Tyr Asn Ser Ile Ile Asn Pro Val Ile Tyr Ala Phe Arg
290     295     300
Asn Gln Glu Ile Gln Lys Ala Leu Cys Leu Ile Cys Cys Gly Cys Ala
305     310     315     320
Ala Ala Arg Gly Arg Thr Pro Pro Ser Leu Gly Pro Gln Asp Glu Ser
325     330     335

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Cys Thr Thr Ala Ser Ser Ser Leu Ala Lys Asp Thr Ser Ser
340 345 350

<210> 45
<211> 1053
<212> DNA
<213> Artificial Sequence

<220>
<223> hGPR12- Enhanced Receptor

<400> 45
atgaatgaag acctgaaggt caatttaagc gggctgcctc gggattatatt agatgccgct 60
gctgcggaga acatctcggc tgctgtctcc tcccgggttc ctgccgtaga gccagagcct 120
gagctcgtag tcaacccctg ggacattgtc ttgtgtacct cgggaaccct catctcctgt 180
gaaaatgcca ttgtgggtcct tatcatcttc cacaacccca gcctgcgagc acccatgttc 240
ctgctaatag gcagcctggc tcttgagac ctgctggccg gcattggact catcaccaat 300
tttgtttttg cctacctgct tcagtcagaa gccaccaagc tggtcacgat cggcctcatt 360
gtgcgctctt tctctgcctc tgtctgcagc ttgttggtta tcactgttga ccgctacctc 420
tcactgtact acgctctgac gtaccattcg gagaggacgg tcacgtttac ctatgtcatg 480
ctcgtcatgc tctgggggac ctccatctgc ctggggctgc tgcccgtcat gggctggaac 540
tgccctccgag acgagtcacac ctgcagcgtg gtcagaccgc tcaccaagaa caacgcggcc 600
atcctctcgg tgcctcttct ctctatgttt gcgctcatgc ttcagctcta catccagatc 660
tgtaagattg tgatgaggca cgcccatcag atagccctgc agcaccactt cctggccacg 720
tcgcactatg tgaccacccg gaaaggggtc tccaccctgg ctatcatcct ggggacgttt 780
gctgcttgct ggatgccttt caccctctat tccttgatag cggattacac ctaccctcc 840
atctatacct acgccaccct cctgcccgcc acctacaatt ccatcatcaa ccctgtcata 900
tatgctttca gaaaccaaga gatccagaaa gcgctctgtc tcatgtgctg cggctgcgcg 960
gccgcacggg gacgcacccc acccagcctg ggtccccaag atgagtcctg caccaccgcc 1020
agctcctccc tggccaagga cacttcatcg tga 1053

<210> 46
<211> 388
<212> PRT
<213> Artificial Sequence

<220>
<223> hSREB3- Enhanced Receptor

<400> 46
Met Ala Asn Thr Thr Gly Glu Pro Glu Glu Val Ser Gly Ala Leu Ser
1 5 10 15
Pro Pro Ser Ala Ser Ala Tyr Val Lys Leu Val Leu Leu Gly Leu Ile
20 25 30
Met Cys Val Ser Leu Ala Gly Asn Ala Ile Leu Ser Leu Leu Val Leu
35 40 45
Lys Glu Arg Ala Leu His Lys Ala Pro Tyr Tyr Phe Leu Leu Asp Leu
50 55 60
Cys Leu Ala Asp Gly Ile Arg Ser Ala Val Cys Phe Pro Phe Val Leu
65 70 75 80
Ala Ser Val Arg His Gly Ser Ser Trp Thr Phe Ser Ala Leu Ser Cys
85 90 95
Lys Ile Val Ala Phe Met Ala Val Leu Phe Cys Phe His Ala Ala Phe
100 105 110
Met Leu Phe Cys Ile Ser Val Thr Arg Tyr Met Ala Ile Ala His His
115 120 125
Arg Phe Tyr Ala Lys Arg Met Thr Leu Trp Thr Cys Ala Ala Val Ile
130 135 140
Cys Met Ala Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Phe
145 150 155 160
Asp Val Gly Thr Tyr Lys Phe Ile Arg Glu Glu Asp Gln Cys Ile Phe
165 170 175

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Glu His Arg Tyr Phe Lys Ala Asn Asp Thr Leu Gly Phe Met Leu Met
 180 185 190
 Leu Ala Val Leu Met Ala Ala Thr His Ala Val Tyr Gly Lys Leu Leu
 195 200 205
 Leu Phe Glu Tyr Arg His Arg Lys Met Lys Pro Val Gln Met Val Pro
 210 215 220
 Ala Ile Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Thr Gly Gln
 225 230 235 240
 Ala Ala Ala Asn Trp Ile Ala Gly Phe Gly Arg Gly Pro Met Pro Pro
 245 250 255
 Thr Leu Leu Gly Ile Arg Gln Asn Gly His Ala Ala Ser Arg Arg Leu
 260 265 270
 Leu Gly Met Asp Glu Val Lys Gly Glu Lys Gln Leu Gly Arg Met Phe
 275 280 285
 Tyr Ala Ile Thr Leu Leu Phe Leu Leu Leu Trp Ser Pro Tyr Ile Val
 290 295 300
 Ala Cys Tyr Trp Arg Val Phe Val Lys Ala Cys Ala Val Pro His Arg
 305 310 315 320
 Tyr Leu Ala Thr Ala Val Trp Met Ser Phe Ala Gln Ala Ala Val Asn
 325 330 335
 Pro Ile Val Cys Phe Leu Leu Asn Lys Asp Leu Lys Lys Cys Leu Arg
 340 345 350
 Thr His Ala Pro Cys Ala Ala Ala Arg Gly Arg Thr Pro Pro Ser Leu
 355 360 365
 Gly Pro Gln Asp Glu Ser Cys Thr Thr Ala Ser Ser Ser Leu Ala Lys
 370 375 380
 Asp Thr Ser Ser
 385

<210> 47
 <211> 1167
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> hSREB3- Enhanced Receptor

<400> 47
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 tcagcttatg tgaagctggg actgctggga ctgattatgt gcgtgagcct ggcgggtaac 120
 gccatcttgt cctgctgggt gctcaaggag cgtgccctgc acaaggctcc ttactacttc 180
 ctgctggacc tgtgcctggc cgatggcata cgctctgccg tctgcttccc ctttgtgctg 240
 gcttctgtgc gccacggctc ttcatggacc ttcatgtcac tcagctgcaa gattgtggcc 300
 tttatggccg tgctcttttg ctccatgacg gccttcatgc tgttctgcat cagcgtcacc 360
 cgctacatgg ccacgcacca ccaccgcttc tacgccaagc gcatgacact ctggacatgc 420
 gcggctgtca tctgcatggc ctggaccctg tctgtggcca tggccttccc acctgtcttt 480
 gacgtgggca cctacaagtt tattcgggag gaggaccagt gcatccttga gcatcgctac 540
 ttcaaggcca atgacacgct gggcttcatg cttatgttgg ctgtgctcat ggcagctacc 600
 catgctgtct acggcaagct gctcctcttc gagtatcgtc accgcaagat gaagccagtg 660
 cagatgggtg cagccatcag ccagaactgg acattccatg gtcccggggc caccggccag 720
 gctgctgcca actggatcgc cggctttggc cgtggggcca tgccaccaac cctgctgggt 780
 atccggcaga atgggcatgc agccagccgg cggctactgg gcatggacga ggtcaagggt 840
 gaaaagcagc tgggcccgcg gttctacgag atcacactgc tctttctgct cctctgggtca 900
 ccctacatcg tggcctgcta ctggcgagtg tttgtgaaag cctgtgctgt gccccaccgc 960
 tacctggcca ctgctgtttg gatgagcttc gccagggctg ccgtcaaccc aattgtctgc 1020
 ttcctgctca acaaggacct caagaagtgc ctgaggactc acgccccctg cgcgcccgca 1080
 cggggacgca cccacccag cctgggtccc caagatgagt cctgcaccac cgccagctcc 1140
 tccctggcca aggacatttc atcgtga 1167

<210> 48
 <211> 388
 <212> PRT

<213> Artificial Sequence

<220>

<223> hSREB2- Enhanced Receptor

<400> 48

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Met Ala Asn Tyr Ser His Ala Ala Asp Asn Ile Leu Gln Asn Leu Ser
 1      5      10      15
Pro Leu Thr Ala Phe Leu Lys Leu Thr Ser Leu Gly Phe Ile Ile Gly
 20      25      30
Val Ser Val Val Gly Asn Leu Leu Ile Ser Ile Leu Leu Val Lys Asp
 35      40      45
Lys Thr Leu His Arg Ala Pro Tyr Tyr Phe Leu Leu Asp Leu Cys Cys
 50      55      60
Ser Asp Ile Leu Arg Ser Ala Ile Cys Phe Pro Phe Val Phe Asn Ser
 65      70      75      80
Val Lys Asn Gly Ser Thr Trp Thr Tyr Gly Thr Leu Thr Cys Lys Val
 85      90      95
Ile Ala Phe Leu Gly Val Leu Ser Cys Phe His Thr Ala Phe Met Leu
100      105      110
Phe Cys Ile Ser Val Thr Arg Tyr Leu Ala Ile Ala His His Arg Phe
115      120      125
Tyr Thr Lys Arg Leu Thr Phe Trp Thr Cys Leu Ala Val Ile Cys Met
130      135      140
Val Trp Thr Leu Ser Val Ala Met Ala Phe Pro Val Leu Asp Val
145      150      155      160
Gly Thr Tyr Ser Phe Ile Arg Glu Glu Asp Gln Cys Thr Phe Gln His
165      170      175
Arg Ser Phe Arg Ala Asn Asp Ser Leu Gly Phe Met Leu Leu Ala
180      185      190
Leu Ile Leu Leu Ala Thr Gln Leu Val Tyr Leu Lys Leu Ile Phe Phe
195      200      205
Val His Asp Arg Arg Lys Met Lys Pro Val Gln Phe Val Ala Ala Val
210      215      220
Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Ser Gly Gln Ala Ala
225      230      235      240
Ala Asn Trp Leu Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Thr Leu
245      250      255
Leu Gly Ile Arg Gln Asn Ala Asn Thr Thr Gly Arg Arg Arg Leu Leu
260      265      270
Val Leu Asp Glu Phe Lys Met Glu Lys Arg Ile Ser Arg Met Phe Tyr
275      280      285
Ile Met Thr Phe Leu Phe Leu Thr Leu Trp Gly Pro Tyr Leu Val Ala
290      295      300
Cys Tyr Trp Arg Val Phe Ala Arg Gly Pro Val Val Pro Gly Gly Phe
305      310      315      320
Leu Thr Ala Ala Val Trp Met Ser Phe Ala Gln Ala Gly Ile Asn Pro
325      330      335
Phe Val Cys Ile Phe Ser Asn Arg Glu Leu Arg Arg Cys Phe Ser Thr
340      345      350
Thr Leu Leu Tyr Cys Ala Ala Ala Arg Gly Arg Thr Pro Pro Ser Leu
355      360      365
Gly Pro Gln Asp Glu Ser Cys Thr Thr Ala Ser Ser Leu Ala Lys
370      375      380
Asp Thr Ser Ser
385

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<210> 49

<211> 1167

<212> DNA

<213> Artificial Sequence

5021US_SEQ.TXT

<220>

<223> hSREB2- Enhanced Receptor

<400> 49

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tttctgaaac tgacttcctt gggtttcata ataggagtca gcgtgggtggg caacctcctg 120
atctccattt tgctagtga agataagacc ttgcatagag caccttacta cttcctgttg 180
gatctttgct gttcagatat cctcagatct gcaatttgtt tcccatttgt gttcaactct 240
gtcaaaaatg gctctacctg gacttatggg actctgactt gcaaagtgat tgcctttctg 300
gggggttttgt cctgtttcca cactgcttct atgctcttct gcatcagtgt caccagatac 360
ttagctatcg cccatcaccg cttctataca aagaggctga ccttttggac gtgtctggct 420
gtgatctgta tgggtgtggac tctgtctgtg gccatggcat ttcccccggt ttagacgtg 480
ggcacttact cattcattag ggaggaagat caatgcacct tccaacaccg ctccttcagg 540
gctaattgatt ccttaggatt tatgctgctt cttgtcttca tcctcctagc cacacagctt 600
gtctacctca agctgatatt tttcgtccac gatcgaagaa aaatgaagcc agtccagttt 660
gtagcagcag tcagccagaa ctggactttt catggctctg gagccagtgg ccaggcagct 720
gccaatggc tagcaggatt tggaaggggt cccacaccac ccacctgtct gggcatcagg 780
caaaatgcaa acaccacagg cagaagaagg ctatttgtct tagacgagtt caaaatggag 840
aaaagaatca gcagaatgtt ctatataatg acttttctgt ttctaaccct gtggggcccc 900
tacctggtgg cctgttattg gagagttttt gcaagagggc ctgtagtacc agggggattt 960
ctaacagctg ctgtctggat gagttttgcc caagcaggaa tcaatcctt tgtctgcatt 1020
ttctcaaaca gggagctgag gcgctgttct agcacaaccc ttctttactg cgcggccgca 1080
cggggacgca cccacccag cctgggtccc caagatgagt cctgcaccac cgccagctcc 1140
tccttgGCCa aggacacttc atcgtga 1167

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<210> 50

<211> 364

<212> PRT

<213> Artificial Sequence

<220>

<223> hGPR8- Enhanced Receptor

<400> 50

```

Met Gln Ala Ala Gly His Pro Glu Pro Leu Asp Ser Arg Gly Ser Phe
1      5      10      15
Ser Leu Pro Thr Met Gly Ala Asn Val Ser Gln Asp Asn Gly Thr Gly
20     25     30
His Asn Ala Thr Phe Ser Glu Pro Leu Pro Phe Leu Tyr Val Leu Leu
35     40     45
Pro Ala Val Tyr Ser Gly Ile Cys Ala Val Gly Leu Thr Gly Asn Thr
50     55     60
Ala Val Ile Leu Val Ile Leu Arg Ala Pro Lys Met Lys Thr Val Thr
65     70     75     80
Asn Val Phe Ile Leu Asn Leu Ala Val Ala Asp Gly Leu Phe Thr Leu
85     90     95
Val Leu Pro Val Asn Ile Ala Glu His Leu Leu Gln Tyr Trp Pro Phe
100    105    110
Gly Glu Leu Leu Cys Lys Leu Val Leu Ala Val Asp His Tyr Asn Ile
115    120    125
Phe Ser Ser Ile Tyr Phe Leu Ala Val Met Ser Val Asp Arg Tyr Leu
130    135    140
Val Val Leu Ala Thr Val Arg Ser Arg His Met Pro Trp Arg Thr Tyr
145    150    155    160
Arg Gly Ala Lys Val Ala Ser Leu Cys Val Trp Leu Gly Val Thr Val
165    170    175
Leu Val Leu Pro Phe Phe Ser Phe Ala Gly Val Tyr Ser Asn Glu Leu
180    185    190
Gln Val Pro Ser Cys Gly Leu Ser Phe Pro Trp Pro Glu Arg Val Trp
195    200    205
Phe Lys Ala Ser Arg Val Tyr Thr Leu Val Leu Gly Phe Val Leu Pro
210    215    220
Val Cys Thr Ile Cys Val Leu Tyr Thr Asp Leu Leu Arg Arg Leu Arg

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225      230      235      240
Ala Val Arg Leu Arg Ser Gly Ala Lys Ala Leu Gly Lys Ala Arg Arg
      245      250      255
Lys Val Thr Val Leu Val Leu Val Val Leu Ala Val Cys Leu Leu Cys
      260      265      270
Trp Thr Pro Phe His Leu Ala Ser Val Val Ala Leu Thr Thr Asp Leu
      275      280      285
Pro Gln Thr Pro Leu Val Ile Ser Met Ser Tyr Val Ile Thr Ser Leu
      290      295      300
Ser Tyr Ala Asn Ser Cys Leu Asn Pro Phe Leu Tyr Ala Phe Leu Asp
305      310      315
Asp Asn Phe Arg Lys Asn Phe Arg Ser Ile Leu Arg Cys Ala Ala Ala
      325      330      335
Arg Gly Arg Thr Pro Pro Ser Leu Gly Pro Gln Asp Glu Ser Cys Thr
      340      345      350
Thr Ala Ser Ser Ser Leu Ala Lys Asp Thr Ser Ser
      355      360

```

<210> 51
 <211> 1095
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> hGPR8- Enhanced Receptor

```

<400> 51
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atgggtgcca acgtctctca ggacaatggc actggccaca atgccacctt ctccgagcca 120
ctgccgttcc tctatgtgct cctgcccgcc gtgtactccg ggatctgtgc tgtggggctg 180
actggcaaca cggccgtcat ccttgaatc ctaaggcgc ccaagatgaa gacggtgacc 240
aacgtgttca tcctgaacct ggccgtcgcc gacgggctct tcacgctggt actgccgctc 300
aacatcgcgg agcacctgct gcagtactgg ccttccgggg agctgctctg caagctggtg 360
ctggccgtcg accactacaa catcttctcc agcatctact tcctagccgt gatgagcgtg 420
gaccgatacc tgggtggtgct ggccaccgtg aggtcccgcc acatgccctg gcgcacctac 480
cggggggcga aggtcgccag cctgtgtgtc tggctgggcg tcacggtcct ggttctgccc 540
ttcttctctt tcgtggcgt ctacagcaac gagctgcagg tccaagctg tgggctgagc 600
ttcccgtggc ccgagcgggt ctggttcaag gccagccgtg tctacacttt ggtcctgggc 660
ttcgtgtctg ccgtgtgcac catctgtgtg ctctacacag acctcctgcg caggctgcgg 720
gccgtgcggc tccgtctctg agccaaggct ctaggcaagg ccaggcggaa ggtgaccgtc 780
ctggtcctcg tcgtgctggc cgtgtgcctc ctctgctgga cgcccttcca cctggcctct 840
gtcgtggccc tgaccacgga cctgccccag accccactgg tcatcagtat gtcctacgtc 900
atcaccagcc tcagctacgc caactcgtgc ctgaaccctt tcctctacgc ctttctagat 960
gacaacttcc ggaagaactt ccgcagcata ttgcggtgcg cggccgcacg gggacgcacc 1020
ccaccagacc tgggtcccca agatgagtc tgcaccaccg ccagctcctc cctggccaag 1080
gacacttcat cgtga

```

<210> 52
 <211> 419
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hGPR22-Enhanced Receptor

```

<400> 52
Met Cys Phe Ser Pro Ile Leu Glu Ile Asn Met Gln Ser Glu Ser Asn
1      5      10      15
Ile Thr Val Arg Asp Asp Ile Asp Asp Ile Asn Thr Asn Met Tyr Gln
20      25      30
Pro Leu Ser Tyr Pro Leu Ser Phe Gln Val Ser Leu Thr Gly Phe Leu
35      40      45

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5021US_SEQ.TXT

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Met Leu Glu Ile Val Leu Gly Leu Gly Ser Asn Leu Thr Val Leu Val
50      55      60
Leu Tyr Cys Met Lys Ser Asn Leu Ile Asn Ser Val Ser Asn Ile Ile
65      70      75      80
Thr Met Asn Leu His Val Leu Asp Val Ile Ile Cys Val Gly Cys Ile
85      90      95
Pro Leu Thr Ile Val Ile Leu Leu Leu Ser Leu Glu Ser Asn Thr Ala
100     105     110
Leu Ile Cys Cys Phe His Glu Ala Cys Val Ser Phe Ala Ser Val Ser
115     120     125
Thr Ala Ile Asn Val Phe Ala Ile Thr Leu Asp Arg Tyr Asp Ile Ser
130     135     140
Val Lys Pro Ala Asn Arg Ile Leu Thr Met Gly Arg Ala Val Met Leu
145     150     155     160
Met Ile Ser Ile Trp Ile Phe Ser Phe Phe Ser Phe Leu Ile Pro Phe
165     170     175
Ile Glu Val Asn Phe Phe Ser Leu Gln Ser Gly Asn Thr Trp Glu Asn
180     185     190
Lys Thr Leu Cys Val Ser Thr Asn Glu Tyr Tyr Thr Glu Leu Gly
195     200     205
Met Tyr Tyr His Leu Leu Val Gln Ile Pro Ile Phe Phe Phe Thr Val
210     215     220
Val Val Met Leu Ile Thr Tyr Thr Lys Ile Leu Gln Ala Leu Asn Ile
225     230     235     240
Arg Ile Gly Thr Arg Phe Ser Thr Gly Gln Lys Lys Lys Ala Arg Lys
245     250     255
Lys Lys Thr Ile Ser Leu Thr Thr Gln His Glu Ala Thr Asp Met Ser
260     265     270
Gln Ser Ser Gly Gly Arg Asn Val Val Phe Gly Val Arg Thr Ser Val
275     280     285
Ser Val Ile Ile Ala Leu Arg Arg Ala Val Lys Arg His Arg Glu Arg
290     295     300
Arg Glu Arg Gln Lys Arg Val Phe Arg Met Ser Leu Leu Ile Ile Ser
305     310     315     320
Thr Phe Leu Leu Cys Trp Thr Pro Ile Ser Val Leu Asn Thr Thr Ile
325     330     335
Leu Cys Leu Gly Pro Ser Asp Leu Leu Val Lys Leu Arg Leu Cys Phe
340     345     350
Leu Val Met Ala Tyr Gly Thr Thr Ile Phe His Pro Leu Leu Tyr Ala
355     360     365
Phe Thr Arg Gln Lys Phe Gln Lys Val Leu Lys Ser Lys Met Lys Lys
370     375     380
Arg Val Val Cys Ala Ala Ala Arg Gly Arg Thr Pro Pro Ser Leu Gly
385     390     395     400
Pro Gln Asp Glu Ser Cys Thr Thr Ala Ser Ser Ser Leu Ala Lys Asp
405     410     415
Thr Ser Ser

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<210> 53

<211> 1260

<212> DNA

<213> Artificial Sequence

<220>

<223> hGPR22-Enhanced Receptor

<400> 53

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atgtgttttt ctccattct ggaaatcaac atgcagtctg aatctaacat tacagtgcga 60
gatgacattg atgacatcaa caccaatatg taccaaccac tatcatatcc gttaagcttt 120
caagtgtctc tcaccggatt tcttatgtta gaaattgtgt tgggacttgg cagcaacctc 180
actgtattgg tactttactg catgaaatcc aacttaatca actctgtcag taacattatt 240

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acaatgaatc ttcattgtact tgatgtaata atttgtgtgg gatgtattcc tctaactata 300
gttatccttc tgcttttact ggagagtaac actgctctca tttgctgttt ccatgaggct 360
tgtgtatctt ttgcaagtgt ctcaacagca atcaacgttt ttgctatcac tttggacaga 420
tatgacatct ctgtaaaacc tgcaaaccga attctgacaa tgggcagagc tgtaattgta 480
atgatatcca tttggatttt ttcttttttc tctttcctga ttctttttat tgaggtaaat 540
tttttcagtc ttcaaagtgg aaatacctgg gaaaacaaga cacttttatg tgtcagtaca 600
aatgaatact acactgaact ggggaatgtat tatcacctgt tagtacagat cccaatattc 660
tttttcactg ttgtagtaat gttaatcaca tacaccaaaa tacttcaggc tcttaatat 720
cgaataggca caagattttc aacagggcag aagaagaaag caagaaagaa aaagacaatt 780
tctctaacca cacaacatga ggctacagac atgtcacaaa gcagtgggtg gagaaatgta 840
gtcttttggtg taagaacttc agtttctgta ataattgccc tccggcgagc tgtgaaacga 900
caccgtgaac gacgagaaag acaaaagaga gtcttcagga tgtctttatt gattatttct 960
acatttcttc tctgctggac accaatttct gttttaaata ccaccatttt atgtttaggc 1020
ccaagtgacc ttttagtaaa attaagattg tgttttttag tcatggctta tggaacaact 1080
atatttcacc ctctattata tgatttact agacaaaaat ttcaaaaggc cttgaaaagt 1140
aaaatgaaaa agcagattgt ttgtgcggcc gcacggggac gcacccacc cagcctgggt 1200
ccccaagatg agtcctgcac caccgccagc tcctccctgg ccaaggacac ttcattcgtga 1260

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<210> 54

<211> 370

<212> PRT

<213> Artificial Sequence

<220>

<223> beta2AR-V2R chimera

<400> 54

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Met Gly Gln Pro Gly Asn Gly Ser Ala Phe Leu Leu Ala Pro Asn Arg
1      5      10      15
Ser His Ala Pro Asp His Asp Val Thr Gln Gln Arg Asp Glu Val Trp
20     25     30
Val Val Gly Met Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val
35     40     45
Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu
50     55     60
Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu
65     70     75     80
Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met
85     90     95
Lys Met Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile
100    105    110
Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala
115    120    125
Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Tyr Gln Ser Leu
130    135    140
Leu Thr Lys Asn Lys Ala Arg Val Ile Ile Leu Met Val Trp Ile Val
145    150    155    160
Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His Trp Tyr Arg Ala
165    170    175
Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Asn Glu Thr Cys Cys Asp
180    185    190
Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser Ile Val Ser Phe
195    200    205
Tyr Val Pro Leu Val Ile Met Val Phe Val Tyr Ser Arg Val Phe Gln
210    215    220
Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu Gly Arg Phe
225    230    235    240
His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly Arg Thr Gly His
245    250    255
Gly Leu Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu His Lys Ala Leu
260    265    270
Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu Cys Trp Leu Pro

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      275      280      285
Phe Phe Ile Val Asn Ile Val His Val Ile Gln Asp Asn Leu Ile Arg
 290      295      300
Lys Glu Val Tyr Ile Leu Leu Asn Trp Ile Gly Tyr Val Asn Ser Gly
 305      310      315
Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe Arg Ile Ala Phe
      325      330      335
Gln Glu Leu Leu Cys Ala Arg Gly Arg Thr Pro Pro Ser Leu Gly Pro
      340      345      350
Gln Asp Glu Ser Cys Thr Thr Ala Ser Ser Ser Leu Ala Lys Asp Thr
      355      360      365
Ser Ser
 370

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<210> 55

<211> 382

<212> PRT

<213> Artificial Sequence

<220>

<223> MOR-V2R chimera

<400> 55

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Met Asp Ser Ser Thr Gly Pro Gly Asn Thr Ser Asp Cys Ser Asp Pro
 1      5      10
Leu Ala Gln Ala Ser Cys Ser Pro Ala Pro Gly Ser Trp Leu Asn Leu
      20      25      30
Ser His Val Asp Gly Asn Gln Ser Asp Pro Cys Gly Leu Asn Arg Thr
      35      40      45
Gly Leu Gly Gly Asn Asp Ser Leu Cys Pro Gln Thr Gly Ser Pro Ser
      50      55      60
Met Val Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val Cys Val
      65      70      75
Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val Arg Tyr
      85      90      95
Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu Ala Leu
      100      105      110
Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val Asn Tyr
      115      120      125
Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile Val Ile
      130      135      140
Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu Cys Thr
      145      150      155
Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys Ala Leu
      165      170      175
Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Val Asn Val Cys Asn Trp
      180      185      190
Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Met Ala Thr Thr
      195      200      205
Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser His Pro
      210      215      220
Thr Trp Tyr Trp Glu Asn Leu Leu Lys Ile Cys Val Phe Ile Phe Ala
      225      230      235
Phe Ile Met Pro Ile Leu Ile Ile Thr Val Cys Tyr Gly Leu Met Ile
      245      250      255
Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu Lys Asp
      260      265      270
Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val Ala Val
      275      280      285
Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile Lys Ala
      290      295      300
Leu Ile Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp His Phe

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5021US_SEQ.TXT

305					310					315				320
Cys	Ile	Ala	Leu	Gly	Tyr	Thr	Asn	Ser	Cys	Leu	Asn	Pro	Val	Leu
				325					330					335
Ala	Phe	Leu	Asp	Glu	Asn	Phe	Lys	Arg	Cys	Phe	Arg	Glu	Phe	Cys
			340					345					350	
Ala	Ala	Arg	Gly	Arg	Thr	Pro	Pro	Ser	Leu	Gly	Pro	Gln	Asp	Glu
		355					360					365		Ser
Cys	Thr	Thr	Ala	Ser	Ser	Ser	Leu	Ala	Lys	Asp	Thr	Ser	Ser	
	370					375					380			

<210> 56
 <211> 382
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> D1AR-V2R chimera

<400> 56														
Met	Ala	Pro	Asn	Thr	Ser	Thr	Met	Asp	Glu	Ala	Gly	Leu	Pro	Ala
1				5				10					15	
Arg	Asp	Phe	Ser	Phe	Arg	Ile	Leu	Thr	Ala	Cys	Phe	Leu	Ser	Leu
			20					25					30	
Ile	Leu	Ser	Thr	Leu	Leu	Gly	Asn	Thr	Leu	Val	Cys	Ala	Ala	Val
		35				40						45		
Arg	Phe	Arg	His	Leu	Arg	Ser	Lys	Val	Thr	Asn	Phe	Phe	Val	Ile
	50					55				60				Ser
Leu	Ala	Val	Ser	Asp	Leu	Val	Ala	Val	Leu	Val	Met	Pro	Trp	Lys
65				70				75						80
Ala	Val	Ala	Glu	Ile	Ala	Gly	Phe	Trp	Pro	Phe	Gly	Ser	Phe	Cys
			85					90					95	Asn
Ile	Trp	Val	Ala	Phe	Asp	Ile	Met	Cys	Ser	Thr	Ala	Ser	Ile	Leu
		100						105					110	Asn
Leu	Cys	Val	Ile	Ser	Val	Asp	Arg	Tyr	Trp	Ala	Ile	Ser	Ser	Pro
		115					120					125		Phe
Gln	Tyr	Glu	Arg	Lys	Met	Thr	Pro	Lys	Ala	Ala	Phe	Ile	Leu	Ile
	130				135						140			Ser
Val	Ala	Trp	Thr	Leu	Ser	Val	Leu	Ile	Ser	Phe	Ile	Pro	Val	Gln
145				150					155					160
Ser	Trp	His	Lys	Lys	Pro	Thr	Trp	Pro	Leu	Asp	Gly	Asn	Phe	Thr
			165					170				175		
Ser	Leu	Glu	Asp	Thr	Glu	Asp	Asp	Asn	Cys	Asp	Thr	Arg	Leu	Ser
		180					185					190		Arg
Thr	Tyr	Ala	Ile	Ser	Ser	Ser	Leu	Ile	Ser	Phe	Tyr	Ile	Pro	Val
	195					200						205		Ala
Ile	Met	Ile	Val	Thr	Tyr	Thr	Ser	Ile	Tyr	Arg	Ile	Ala	Gln	Lys
	210					215					220			Gln
Ile	Arg	Arg	Ile	Ser	Ala	Leu	Glu	Arg	Ala	Ala	Val	His	Ala	Lys
225					230				235					240
Cys	Gln	Thr	Thr	Ala	Gly	Asn	Gly	Asn	Pro	Val	Glu	Cys	Ala	Gln
			245						250				255	Ser
Glu	Ser	Ser	Phe	Lys	Met	Ser	Phe	Lys	Arg	Glu	Thr	Lys	Val	Leu
		260					265					270		Lys
Thr	Leu	Ser	Val	Ile	Met	Gly	Val	Phe	Val	Cys	Cys	Trp	Leu	Pro
	275					280						285		Phe
Phe	Ile	Ser	Asn	Cys	Met	Val	Pro	Phe	Cys	Gly	Ser	Glu	Glu	Thr
	290				295					300				Gln
Pro	Phe	Cys	Ile	Asp	Ser	Ile	Thr	Phe	Asp	Val	Phe	Val	Trp	Phe
305				310					315					Gly
Trp	Ala	Asn	Ser	Ser	Leu	Asn	Pro	Ile	Ile	Tyr	Ala	Phe	Asn	Ala
			325						330				335	Asp
Phe	Gln	Lys	Ala	Phe	Ser	Thr	Leu	Leu	Gly	Cys	Tyr	Arg	Leu	Cys

5021US_SEQ.TXT

Ala Ala Arg Gly Arg Thr Pro Pro Ser Leu Gly Pro Gln Asp Glu Ser
 340 355 360 365 350
 Cys Thr Thr Ala Ser Ser Ser Leu Ala Lys Asp Thr Ser Ser
 370 375 380

<210> 57

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> 5HT1AR-V2R chimera

<400> 57

Met Asp Val Leu Ser Pro Gly Gln Gly Asn Asn Thr Thr Ser Pro Pro
 1 5 10 15
 Ala Pro Phe Glu Thr Gly Gly Asn Thr Thr Gly Ile Ser Asp Val Thr
 20 25 30
 Val Ser Tyr Gln Val Ile Thr Ser Leu Leu Leu Gly Thr Leu Ile Phe
 35 40 45
 Cys Ala Val Leu Gly Asn Ala Cys Val Val Ala Ala Ile Ala Leu Glu
 50 55 60
 Arg Ser Leu Gln Asn Val Ala Asn Tyr Leu Ile Gly Ser Leu Ala Val
 65 70 75 80
 Thr Asp Leu Met Val Ser Val Leu Val Leu Pro Met Ala Ala Leu Tyr
 85 90 95
 Gln Val Leu Asn Lys Trp Thr Leu Gly Gln Val Thr Cys Asp Leu Phe
 100 105 110
 Ile Ala Leu Asp Val Leu Cys Cys Thr Ser Ser Ile Leu His Leu Cys
 115 120 125
 Ala Ile Ala Leu Asp Arg Tyr Trp Ala Ile Thr Asp Pro Ile Asp Tyr
 130 135 140
 Val Asn Lys Arg Thr Pro Arg Arg Ala Ala Ala Leu Ile Ser Leu Thr
 145 150 155 160
 Trp Leu Ile Gly Phe Leu Ile Ser Ile Pro Pro Met Leu Gly Trp Arg
 165 170 175
 Thr Pro Glu Asp Arg Ser Asp Pro Asp Ala Cys Thr Ile Ser Lys Asp
 180 185 190
 His Gly Tyr Thr Ile Tyr Ser Thr Phe Gly Ala Phe Tyr Ile Pro Leu
 195 200 205
 Leu Leu Met Leu Val Leu Tyr Gly Arg Ile Phe Arg Ala Ala Arg Phe
 210 215 220
 Arg Ile Arg Lys Thr Val Lys Lys Val Glu Lys Thr Gly Ala Asp Thr
 225 230 235 240
 Arg His Gly Ala Ser Pro Ala Pro Gln Pro Lys Lys Ser Val Asn Gly
 245 250 255
 Glu Ser Gly Ser Arg Asn Trp Arg Leu Gly Val Glu Ser Lys Ala Gly
 260 265 270
 Gly Ala Leu Cys Ala Asn Gly Ala Val Arg Gln Gly Asp Asp Gly Ala
 275 280 285
 Ala Leu Glu Val Ile Glu Val His Arg Val Gly Asn Ser Lys Glu His
 290 295 300
 Leu Pro Leu Pro Ser Glu Ala Gly Pro Thr Pro Cys Ala Pro Ala Ser
 305 310 315 320
 Phe Glu Arg Lys Asn Glu Arg Asn Ala Glu Ala Lys Arg Lys Met Ala
 325 330 335
 Leu Ala Arg Glu Arg Lys Thr Val Lys Thr Leu Gly Ile Ile Met Gly
 340 345 350
 Thr Phe Ile Leu Cys Trp Leu Pro Phe Phe Ile Val Ala Leu Val Leu
 355 360 365
 Pro Phe Cys Glu Ser Ser Cys His Met Pro Thr Leu Leu Gly Ala Ile

5021US_SEQ.TXT

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      370      375      380
Ile Asn Trp Leu Gly Tyr Ser Asn Ser Leu Leu Asn Pro Val Ile Tyr
385      390      395      400
Ala Tyr Phe Asn Lys Asp Phe Gln Asn Ala Phe Lys Lys Ile Ile Lys
      405      410      415
Cys Asn Phe Cys Ala Ala Ala Arg Gly Arg Thr Pro Pro Ser Leu Gly
      420      425      430
Pro Gln Asp Glu Ser Cys Thr Thr Ala Ser Ser Ser Leu Ala Lys Asp
      435      440      445
Thr Ser Ser
      450

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<210> 58

<211> 394

<212> PRT

<213> Artificial Sequence

<220>

<223> beta3AR-V2R chimera

<400> 58

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Met Ala Pro Trp Pro His Glu Asn Ser Ser Leu Ala Pro Trp Pro Asp
1      5      10      15
Leu Pro Thr Leu Ala Pro Asn Thr Ala Asn Thr Ser Gly Leu Pro Gly
      20      25      30
Val Pro Trp Glu Ala Ala Leu Ala Gly Ala Leu Leu Ala Leu Ala Val
      35      40      45
Leu Ala Thr Val Gly Gly Asn Leu Leu Val Ile Val Ala Ile Ala Trp
      50      55      60
Thr Pro Arg Leu Gln Thr Met Thr Asn Val Phe Val Thr Ser Leu Ala
      65      70      75      80
Ala Ala Asp Leu Val Met Gly Leu Leu Val Val Pro Pro Ala Ala Thr
      85      90      95
Leu Ala Leu Thr Gly His Trp Pro Leu Gly Ala Thr Gly Cys Glu Leu
      100      105      110
Trp Thr Ser Val Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu
      115      120      125
Cys Ala Leu Ala Val Asp Arg Tyr Leu Ala Val Thr Asn Pro Leu Arg
      130      135      140
Tyr Gly Ala Leu Val Thr Lys Arg Cys Ala Arg Thr Ala Val Val Leu
      145      150      155      160
Val Trp Val Val Ser Ala Ala Val Ser Phe Ala Pro Ile Met Ser Gln
      165      170      175
Trp Trp Arg Val Gly Ala Asp Ala Glu Ala Gln Arg Cys His Ser Asn
      180      185      190
Pro Arg Cys Cys Ala Phe Ala Ser Asn Met Pro Tyr Val Leu Leu Ser
      195      200      205
Ser Ser Val Ser Phe Tyr Leu Pro Leu Leu Val Met Leu Phe Val Tyr
      210      215      220
Ala Arg Val Phe Val Val Ala Thr Arg Gln Leu Arg Leu Leu Arg Gly
      225      230      235      240
Glu Leu Gly Arg Phe Pro Pro Glu Glu Ser Pro Pro Ala Pro Ser Arg
      245      250      255
Ser Leu Ala Pro Ala Pro Val Gly Thr Cys Ala Pro Pro Glu Gly Val
      260      265      270
Pro Ala Cys Gly Arg Arg Pro Ala Arg Leu Leu Pro Leu Arg Glu His
      275      280      285
Arg Ala Leu Cys Thr Leu Gly Leu Ile Met Gly Thr Phe Thr Leu Cys
      290      295      300
Trp Leu Pro Phe Phe Leu Ala Asn Val Leu Arg Ala Leu Gly Gly Pro
      305      310      315      320
Ser Leu Val Pro Gly Pro Ala Phe Leu Ala Leu Asn Trp Leu Gly Tyr

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5021US_SEQ.TXT

325 330 335
 Ala Asn Ser Ala Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe
 340 345 350
 Arg Ser Ala Phe Arg Arg Leu Leu Cys Arg Cys Ala Ala Arg Gly
 355 360 365
 Arg Thr Pro Pro Ser Leu Gly Pro Gln Asp Glu Ser Cys Thr Thr Ala
 370 375 380
 Ser Ser Ser Leu Ala Lys Asp Thr Ser Ser
 385 390

<210> 59
 <211> 362
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Edg1R-V2R chimera

<400> 59
 Met Gly Pro Thr Ser Val Pro Leu Val Lys Ala His Arg Ser Ser Val
 1 5 10 15
 Ser Asp Tyr Val Asn Tyr Asp Ile Ile Val Arg His Tyr Asn Tyr Thr
 20 25 30
 Gly Lys Leu Asn Ile Ser Ala Asp Lys Glu Asn Ser Ile Lys Leu Thr
 35 40 45
 Ser Val Val Phe Ile Leu Ile Cys Cys Phe Ile Ile Leu Glu Asn Ile
 50 55 60
 Phe Val Leu Leu Thr Ile Trp Lys Thr Lys Lys Phe His Arg Pro Met
 65 70 75 80
 Tyr Tyr Phe Ile Gly Asn Leu Ala Leu Ser Asp Leu Leu Ala Gly Val
 85 90 95
 Ala Tyr Thr Ala Asn Leu Leu Leu Ser Gly Ala Thr Thr Tyr Lys Leu
 100 105 110
 Thr Pro Ala Gln Trp Phe Leu Arg Glu Gly Ser Met Phe Val Ala Leu
 115 120 125
 Ser Ala Ser Val Phe Ser Leu Leu Ala Ile Ala Ile Glu Arg Tyr Ile
 130 135 140
 Thr Met Leu Lys Met Lys Leu His Asn Gly Ser Asn Asn Phe Arg Leu
 145 150 155 160
 Phe Leu Leu Ile Ser Ala Cys Trp Val Ile Ser Leu Ile Leu Gly Gly
 165 170 175
 Leu Pro Ile Met Gly Trp Asn Cys Ile Ser Ala Leu Ser Ser Cys Ser
 180 185 190
 Thr Val Leu Pro Leu Tyr His Lys His Tyr Ile Leu Phe Cys Thr Thr
 195 200 205
 Val Phe Thr Leu Leu Leu Leu Ser Ile Val Ile Leu Tyr Cys Arg Ile
 210 215 220
 Tyr Ser Leu Val Arg Thr Arg Ser Arg Arg Leu Thr Phe Arg Lys Asn
 225 230 235 240
 Ile Ser Lys Ala Ser Arg Ser Ser Glu Lys Ser Leu Ala Leu Leu Lys
 245 250 255
 Thr Val Ile Ile Val Leu Ser Val Phe Ile Ala Cys Trp Ala Pro Leu
 260 265 270
 Phe Ile Leu Leu Leu Leu Asp Val Gly Cys Lys Val Lys Thr Cys Asp
 275 280 285
 Ile Leu Phe Arg Ala Glu Tyr Phe Leu Val Leu Ala Val Leu Asn Ser
 290 295 300
 Gly Thr Asn Pro Ile Ile Tyr Thr Leu Thr Asn Lys Glu Met Arg Arg
 305 310 315 320
 Ala Phe Ile Arg Ile Met Ser Cys Cys Lys Cys Ala Ala Arg Gly
 325 330 335
 Arg Thr Pro Pro Ser Leu Gly Pro Gln Asp Glu Ser Cys Thr Thr Ala

5021US_SEQ.TXT 350
340
Ser Ser Ser Leu Ala Lys Asp Thr Ser Ser
355 360